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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=14; hr=18; min=42; sec=41; ms=906; ]

=====

\*\*\*\*\*

Reviewer Comments:

<210> 3

<211> 951

<212> DNA

<213> Mouse

Per 1.823 of the Sequence Rules, the only valid <213> responses are: the Genus species of the organism, "Artificial Sequence," or "Unknown." "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section. Please give the Genus species. This response appears in subsequent sequences.

<210> 9

<211> 1670

<212> DNA

<213> Chimera

The above <213> response is invalid: since this is a chimeric sequence, please use "Artificial Sequence," and give the sources in the <220>-<223> section. Same response in subsequent sequences.

\*\*\*\*\*

Application No: 10824481 Version No: 2.0

Input Set:

Output Set:

Started: 2008-03-04 15:06:46.434  
Finished: 2008-03-04 15:06:48.842  
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 408 ms  
Total Warnings: 30  
Total Errors: 0  
No. of SeqIDs Defined: 35  
Actual SeqID Count: 35

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)

**Input Set:**

**Output Set:**

**Started:** 2008-03-04 15:06:46.434  
**Finished:** 2008-03-04 15:06:48.842  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 408 ms  
**Total Warnings:** 30  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 35  
**Actual SeqID Count:** 35

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34) This error has occurred more than 20 times, will not be displayed

# SEQUENCE LISTING

<110> Wyeth  
Ling, Vincent  
Carreno, Beatriz M.  
Collins, Mary

<120> USE OF B7-H3 TO INHIBIT LYMPHOCYTE PROLIFERATION (As Amended)

<130> 08702.6108-00000

<140> 10824481

<141> 2004-04-15

<160> 35

<170> PatentIn version 3.5

<210> 1

<211> 951

<212> DNA

<213> Homo sapiens

<400> 1

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ctggtgggca ccgatgccac cctgtgctgc tccttctccc ctgagcctgg cttcagcctg	180
gcacagctca acctcatctg gcagctgaca gataccaaac agctggtgca cagctttgct	240
gagggccagg accagggcag cgcttatgcc aaccgcacgg ccctcttccc ggacctgctg	300
gcacagggca acgcatccct gaggtgagcag cgcgtgcgtg tggcggacga gggcagcttc	360
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<210> 2  
<211> 316  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly Ala  
1 5 10 15

Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln  
20 25 30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu  
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn  
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala  
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe  
85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val  
100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp  
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys  
130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr  
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val  
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr  
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu

195

200

205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn  
 210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln  
 225 230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser  
 245 250 255

Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg  
 260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln  
 275 280 285

Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro Leu Lys His  
 290 295 300

Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala  
 305 310 315

<210> 3  
 <211> 951  
 <212> DNA  
 <213> Mouse

<400> 3  
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 ctggtggaca cggatgccac cctacgtgc tccttttccc cagagcctgg cttcagtctg 180  
 gcacagctca acctcatctg gcagctgaca gacaccaaac agctggtgca cagcttcacg 240  
 gagggccggg accaaggcag tgcctactcc aaccgcacag cgctcttccc tgacctgttg 300  
 gtgcaaggca atgcgtcctt gaggtgtcag cgcgtccgag taaccgacga gggcagctac 360  
 acctgctttg tgagcatcca ggactttgac agcgtgtgtg ttagcctgca ggtggccgcc 420  
 ccctactcga agcccagcat gaccctggag cccaacaagg acctacgtcc agggaaacatg 480  
 gtgaccatca cgtgctctag ctaccagggc tatccggagg ccgaggtgtt ctggaaggat 540  
 ggacaggagg tgccttgac tggcaatgtg accacatccc agatggccaa cgagcggggc 600

ttgttcgatg ttcacagcgt gctgaggggtg gtgctgggtg ctaacggcac ctacagctgc	660
ctggtacgca acccgggtgtt gcagcaagat gctcacggct cagtcaccat cacagggcag	720
cccttgacat tccccctga ggctctgtgg gtaaccgtgg ggctctctgt ctgtcttgtg	780
gtactactgg tggccttggc tttcgtgtgc tggagaaaga tcaagcagag ctgcgaggag	840
gagaatgcag gtgccgagga ccaggatgga gatggagaag gatccaagac agctctacgg	900
cctctgaaac cctctgaaaa caaagaagat gacggacaag aaattgcttg a	951

<210> 4  
 <211> 316  
 <212> PRT  
 <213> Mouse

<400> 4

Met	Leu	Arg	Gly	Trp	Gly	Gly	Pro	Ser	Val	Gly	Val	Cys	Val	Arg	Thr
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Ala	Leu	Gly	Val	Leu	Cys	Leu	Cys	Leu	Thr	Gly	Ala	Val	Glu	Val	Gln
			20					25					30		

Val	Ser	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Asp	Thr	Asp	Ala	Thr	Leu
		35						40				45			

Arg	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn
	50					55					60				

Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Thr
65					70				75						80

Glu	Gly	Arg	Asp	Gln	Gly	Ser	Ala	Tyr	Ser	Asn	Arg	Thr	Ala	Leu	Phe
				85						90				95	

Pro	Asp	Leu	Leu	Val	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	Val
		100						105					110		

Arg	Val	Thr	Asp	Glu	Gly	Ser	Tyr	Thr	Cys	Phe	Val	Ser	Ile	Gln	Asp
		115					120					125			

Phe	Asp	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys
	130					135						140			

Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asn	Met
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val  
165 170 175

Phe Trp Lys Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr  
180 185 190

Ser Gln Met Ala Asn Glu Arg Gly Leu Phe Asp Val His Ser Val Leu  
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn  
210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln  
225 230 235 240

Pro Leu Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser  
245 250 255

Val Cys Leu Val Val Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg  
260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln  
275 280 285

Asp Gly Asp Gly Glu Gly Ser Lys Thr Ala Leu Arg Pro Leu Lys Pro  
290 295 300

Ser Glu Asn Lys Glu Asp Asp Gly Gln Glu Ile Ala  
305 310 315

<210> 5  
<211> 1605  
<212> DNA  
<213> Homo sapiens

<400> 5  
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ctggtgggca ccatgccac cctgtgctgc tccttctccc ctgagcctgg cttcagcctg 180  
gcacagctca acctcatctg gcagctgaca gataccaaac agctgggtgca cagctttgct 240



Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly Ala  
1 5 10 15

Ala	Leu	Gly	Ala	Leu	Trp	Phe	Cys	Leu	Thr	Gly	Ala	Leu	Glu	Val	Gln	20	25	30
Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	Ala	Thr	Leu	35	40	45
Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn	50	55	60
Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Ala	65	70	75
Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	Asn	Arg	Thr	Ala	Leu	Phe	85	90	95
Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	Val	100	105	110
Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	115	120	125
Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	130	135	140
Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	145	150	155
Val	Thr	Ile	Thr	Cys	Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	165	170	175
Phe	Trp	Gln	Asp	Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	180	185	190
Ser	Gln	Met	Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Ile	Leu	195	200	205
Arg	Val	Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	210	215	220
Pro	Val	Leu	Gln	Gln	Asp	Ala	His	Ser	Ser	Val	Thr	Ile	Thr	Pro	Gln	225	230	235
																		240

Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val  
245 250 255

Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro  
260 265 270

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr  
275 280 285

Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly  
290 295 300

Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln  
305 310 315 320

Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly  
325 330 335

Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val  
340 345 350

Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu  
355 360 365

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser  
370 375 380

Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln  
385 390 395 400

Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu  
405 410 415

Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala  
420 425 430

Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp  
435 440 445

Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro  
450 455 460

Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu

465 470 475 480

Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys  
485 490 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly  
500 505 510

Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp  
515 520 525

Asp Gly Gln Glu Ile Ala  
530

<210> 7  
<211> 112  
<212> PRT  
<213> Homo sapience

<400> 7

Ala Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly  
1 5 10 15

Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser  
20 25 30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu  
35 40 45

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn  
50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu  
65 70 75 80

Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe  
85 90 95

Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala  
100 105 110

<210> 8  
<211> 112  
<212> PRT

<213> Homo sapiens

<220>

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<222> (2)..(2)

<223> L, or V, or any other amino acid

<220>

<221> MISC\_FEATURE

<222> (22)..(22)

<223> C, or R, or any other amino acid

<220>

<221> MISC\_FEATURE

<222> (53)..(53)

<223> A, or T, or any other amino acid

<220>

<221> MISC\_FEATURE

<222> (56)..(56)

<223> Q, or R, or any other amino acid

<400> 8

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Thr Asp Ala Thr Leu Xaa Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser  
20 25 30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu  
35 40 45

Val His Ser Phe Xaa Glu Gly Xaa Asp Gln Gly Ser Ala Tyr Ala Asn  
50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu  
65 70 75 80

Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe  
85 90 95

Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala  
100 105 110

<210> 9

<211> 1670

<212> DNA

<213> Chimera

<400> 9

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